

[illegible]

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h: 1 MSGSTQPVAAQTWRATEPRYPHSLSYPVQIARTHTDVGLEYQHHSRDYASHLSPGSI IQPQRRRPSLLSEFQPGNERSQELHLRPESHSLYLPGLGKXSM
m: 1 -----A-----GI-----S-----P-----T-----S-----RTF-----PDI

h: 101 EFIESKRPRLELLPDPLLRLPSPLLATGQPAGSEDLTKDRSLTGKLEFVSPSPPHDTPELELVPPRLSKEELIQN.MDRVDREITMVEQQISKLKKKQQQ
m: 101 --T-----T-----S-----A-----A-----A-S-----RL-----

h: 200 LEEEAAPPEPEKPVSPPIESKHSRLVQIIYDENRKKAAEAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWEQKFC
m: 201 -----R-----

h: 300 QRYDQLMEAWKVERIENPNRRRAKESKVREYYEQFPFIRKQRELQERMQ.RVGQRGSGLSMSPARSEHEVSEIIDGLSEQENLEKQMRQLAVIPMML
m: 301 -----S-----A-----RHV

h: 399 YDADQQRIRKFINMNGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKNFGLIASFLERKTVACVLYYYLTCKNENYKSLVRRSYRRRGKSQQQQQQ
m: 401 .RR-----D-----T-----RD-----

h: 499 QQQQQQQQQQMPRSSQEEKDEKEKEKEAEKEEKEPEVENDKEDLLKEKTDSTSGEDNDEKEAVASKRKTANSQGRRKGRITRSMANEANSEEAITPQ
m: 500 -----A-----E-----D-----QDA--E--E-S-----H-TA--

h: 599 QSaelasmelnessrwteemetaKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRQNLDEILQHQHKLKMEKERNARRKKKAPAAASEEAFFPV
m: 596 --S-----M-----T-----A
m: AC: --S-----M-----HQTGPGGARLLTQQELRAPIPSTPQLQPHSHRPHPSKEPCTPPCQSGPAGAHGLRSAPRKDSK*

h: 699 VEDEEMEASGVTGNEEEMVEEAET.....VNNSSDTEsIPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPPEDIPAPTESTP
m: 696 A-----SA-----LA-----SQASGNEVPRVGECSGPA-----V--RS--T-----G-EALPAATQP-VP--E-PAA--A-PS-

h: 781 ASEATLAPTPPPAPPFPSSPPVVPKKEEKEETAAAPFVEEGEQKPPAAEELAVDTGKAEPP.....VKSECTEEAEEGPA.KGKDAEAAEATAE
m: 793 VPD-SGPPS-E-S-S.-AA--AT-D-D-Q-APA-P--QT-DAK--SEAE...I-V--P--EASEEPPES--DHK--T--E-ED-A-GT--I-TVS-

h: 871 RALKAekEGGSGRATTAKSSGAPQDSsSATCSADEVDEAEGGDKNRLLSPRPSLLTPTGDPRANASPKPLDLKQLKQRAAIIPIQVTKVHEPPRED
m: 889 AP--V-.EAGSKAAV-KGS--T-----P-----G-----A-----ST-----

MEAWDAH-P->(SMRT)

h: 971 AAPTkpAPPAPPPQNLQPESDAPQQPGSSPRGKSRSAPPADKEAKPVFFPAFAAEBAQKLPGDPPCWTSGLFFPVPPREVIKASPHAPDPSAFSYAPP
m: 987 TV-P-V-V--T-H--G-VS--S-G-----V--E-----A-----PT-G-SYRLS-HA.GHR--.SH-----T-TR--.L--T--

h: 1071 GHPLPLGLHDTARPVLP RPPTISNPPPLISSAKHPSVLERQIGAISQGMsvQLHVPYSEHAKAPVGPVTMGLPLPMDPKKLAPFSGVKQEQLSPRGQAGP
m: 1083 -----S-----G-----R-H-----M-L-E--AV-----GTALAPPVEA--ASQ..

h: 1171 PESLGVPTAQEASVLRGTALGSVPGGSITKGIPTSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIEGKKGHVLSY
m: 1179 .....Y-GC-R-QLQRLYH....PR-----S-V-----A--T-----

h: 1271 EGGMSVTQCSKEDGRSSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGLMGRAIPPERHSPHHLKEQHHRGSITQGI PRSYVEAQEDYLREAKLLKR
m: 1243 -----S-----TVT-----Q-----

h: 1371 EGTppppPSRDLTEAYKTQ...ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSITQGTPLKYDTGASTTGSKKHDVRSLI
m: 1341 -----P-----T--PRPLDP-----T--V-----R-----S--PS--T-----

h: 1468 GSPGRTFPPVHPLDVMADARALERACyEESLKSrPGTASSSGGSiARGAPVIVPELGKPRQSPLTYEDHGAPFAGHLPRGSPVTMREPTPRLQEGSLSSS
m: 1441 -----P--AL-----I-----S--S-GA--T--V-----TS-----T-----L--

h: 1568 KASQDRKLTSTPREIAKSPHSTVPEHHPIISPYEHLRrGVSGVDLYRSHIPLAFDPTSIPRGIPLD.AAAAYYLPRHLAPNPTYPHLYPPYLIRGYPDT
m: 1541 -----T-----G-----EA-----S-----

M->(TRAC1)

h: 1667 AALENRQTIINDYITSQMHHTATAMAQRADMLRGLSPRESSLALNYAAGPRGIIIDLSQVPHLPVLVPPTPGTPATAMDRLAYLPTAPQPFSSRHSSSP
m: 1641 -----A-S-----S-----I-----P--H--

h: 1767 LSPGGPthLTkPTTTSSSERERDRDRERDREREKSILtSTTtVehAPIWRPGTEQSSGSSGSSGGGGSSSRPASHSHAHQHSPIsPRTQDALQQRPS
m: 1741 -----A--A-----E-E-----G-----

h: 1867 VLHNTGMKGIIITAVEPSKPTVLRSTSTSSPVRPAATFPFATHCPLGGTLdGVYPTLMEPVLLPKAEPRVARPERPRADTGHAFLAKPPARSGLEPASSPS
m: 1825 -----S--VV-S--GT-----E-----TS-----V-G--T-----

h: 1967 KGSEPRPLVPPVSGHATIARTPAKNLAPHHASPDPPAPPASADPHREKTOSKPFsIQELeLRSLGyH.GSSYSPEGVEPVSPVSSPSLTHDKGLPKHLE
m: 1922 -S---S-A--S-S-TA-----S-----G.-T--L-----S-AG--D--I-----S-P--

h: 2066 ELdkshLEGELRPKQPGPVKLGEAAHLPHLRPLPESQPSsPllQTAPGVKGhQRVVTLaQHISEViTQDYTRHHPQQLSAPLPAPLYSFPGASCPVLD
m: 2021 --E-----H-----M--SA-----I-----G-----

h: 2166 LRRPPSDLYLPPPDHGAPARGSPHSEGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTepGHSRSaVYPLLYRDGEQTEPSRMGSKSPGNTSQPPAFFSKL
m: 2121 -----T-----S-----SS-A-----A-----G-----

h: 2266 TESNSAMVSKKQEIINKLNTNHRNEPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESPLSANAFNPLNASa
m: 2220 -----G-----A--C-----P--G-----

h: 2366 SLP.AAMPITAADGRSDHTLTSPGGGGKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVWEDRPSSAGSTFPFYNPLIMRLQAG
m: 2320 --A-----T-----A-----

h: 2465 VMASPPPPGLPAGSGPLAGPHHAWDEEPKLLCSQYETLSDSE 2507
m: 2420 -----A-----2462

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Fig. 2

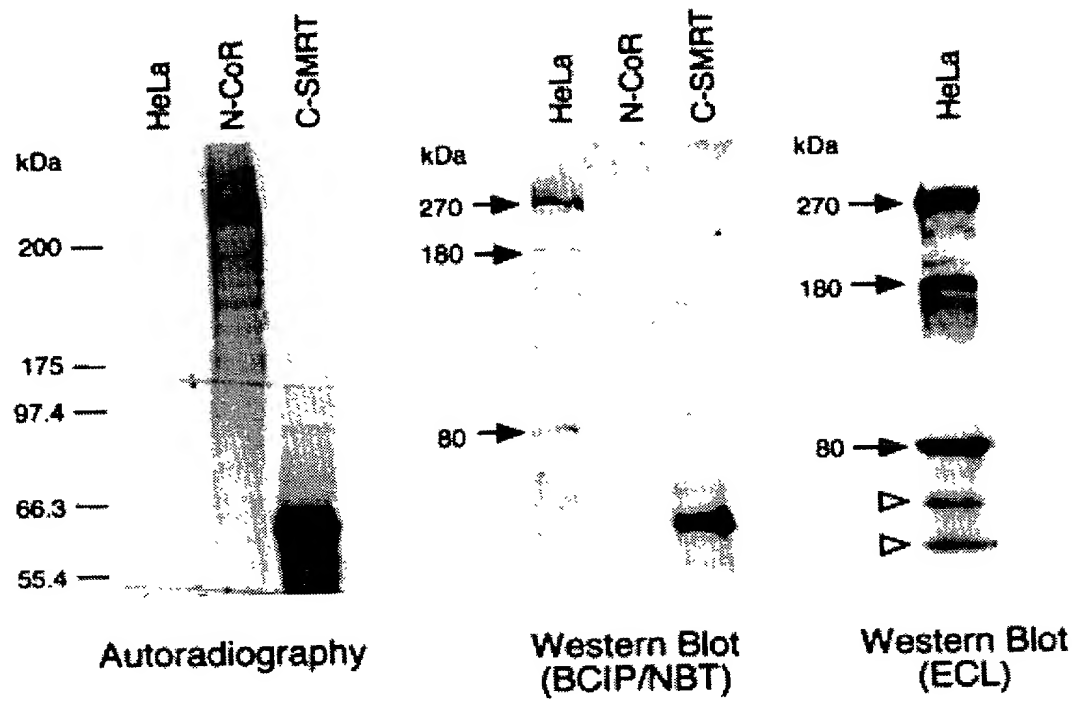
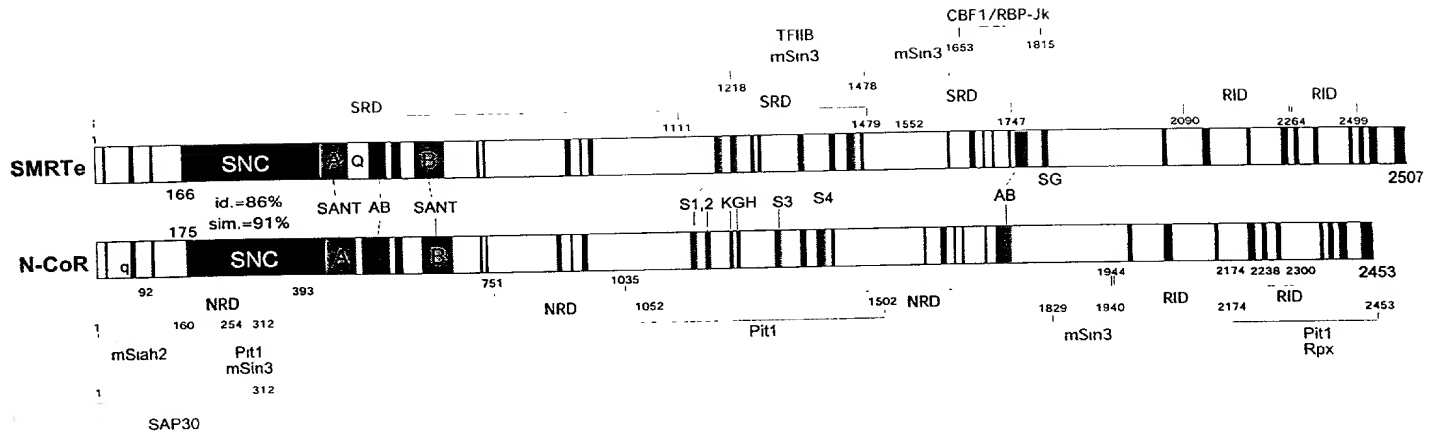


Fig. 3



106220-106230

Fig. 4

hS 166 RLSKEELIQN.MDRVDREITMVEQQISKLKKKQQQLEEEAAKPPEPEKPV
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mN 175 RLSKEELIQS.MDRVDREITAKVEQQILKLKKKQQQLEEEAAKPPEPEKPV

hS 215 SPPPIESKHRSIVQIIYDENRKKAEAAHRIEGLGPQVELPLYNQPSDTR
mS 216 SPPPIESKHRSIVQIIYDENRKKAEAAHRIEGLGPQVELPLYNQPSDTR
hN 224 SPPPIVEQKHRSIVQIIYDENRKKAEAAHRIEGLGPKVELPLYNQPSDTK
mN 224 SPPPIVEQKHRSIVQIIYDENRKKAEAAHRIEGLGPKVELPLYNQPSDTK

hS 265 QYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEAWKEKKVE
mS 266 QYHENIKINQAMRKKLILYFKRRNHARKQWEQKFCORYDQLEAWKEKKVE
hN 274 VYHENIKINQVMRKKLILYFKRRNHARKQWEQKFCORYDQLEAWKEKKVD
mN 274 VYHENIKINQVMRKKLILYFKRRNHARKQWEQKFCORYDQLEAWKEKKVD

hS 315 RIENNPRRRAKESKVREYYEKQFPEIRKQRELOQERMO.RVGQRGSGLSMS
mS 316 RIENNPRRRAKESKVREYYEKQFPEIRKQRELOQERMOSRVGQRGSGLSMS
hN 324 RIENNPRRRAKESKVREYYEKQFPEIRKQRELOQERFO.RVGQRGAGLSAT
mN 324 RIENNPRRRAKESKVREYYEKQFPEIRKQRELOQERFO.RVGQRGAGLSAT

hS 364 PARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMILYDADQORIKFINMNG
mS 366 AARSEHEVSEIIDGLSEQENLEKQMRQLAVIRHVY.RRDOQORIKFINMNG
hN 373 IARSEHEVSEIIDGLSEQENNEKQMRQLSVIPPMIFDAEQRRVYKFINMNG
mN 373 IARSEHEVSEIIDGLSEQENNEKQMRQLSVIPPMIFDAEQRRVYKFINMNG

hS 414 LMA DPMKVYKDRQVMN
mS 415 LMA DPMKVYKDRQVTN
hN 423 LMA DPMKVYKDRQFMN
mN 423 LMA DPMKVYKDRQFMN

SANT "A"

hSMRte-A 430 MWSEQEKETFREKFMQHPKNFGLIASFLERKTVAECVLYYYLTKKNNENYKSLVRRSY
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hNCoR-A 439 MWSEHEKEIFRKKEFQHPKNFGLIASFLERKSVPCVLYYYLTKKNNENYKSLVRRSY
mNCoR-A 439 MWSEHEKEIFRKKEFQHPKNFGLIASFLERKSVPCVLYYYLTKKNNENYKSLVRRSY
hSMRte-B 613 RWTEBEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRONLDEILQOHK

Myb Signatures: WSxxEDxxxx WxxIAxxxxxxRxxxxxxxxxWxxx
Myb Structure: hhhhhhhhhhhhhhh hhhhhhh hhhhhhhhhhh

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hNCoR-B 613 RWTEBEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRONLDEILQOHK
mNCoR-B 622 RWTEBEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYFNYKKRONLDEILQOHK
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SANT "B"

Fig. 5

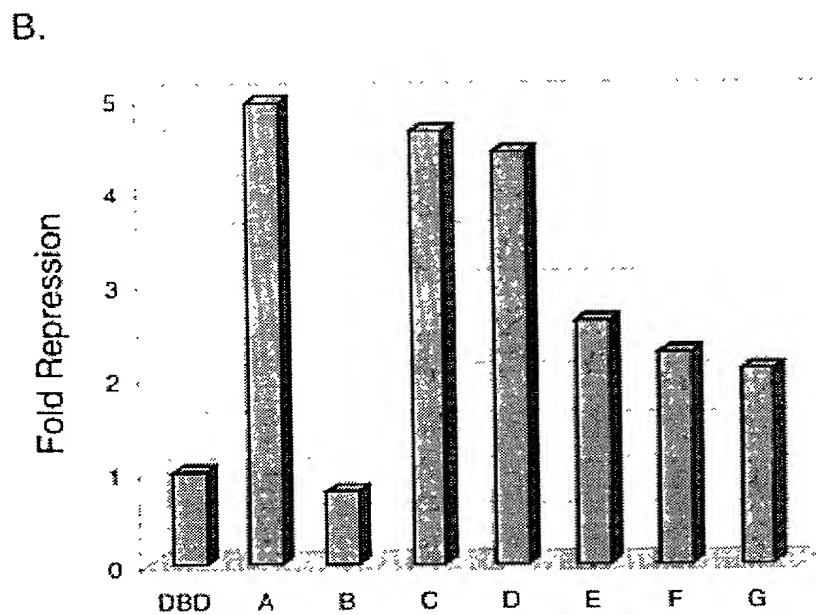
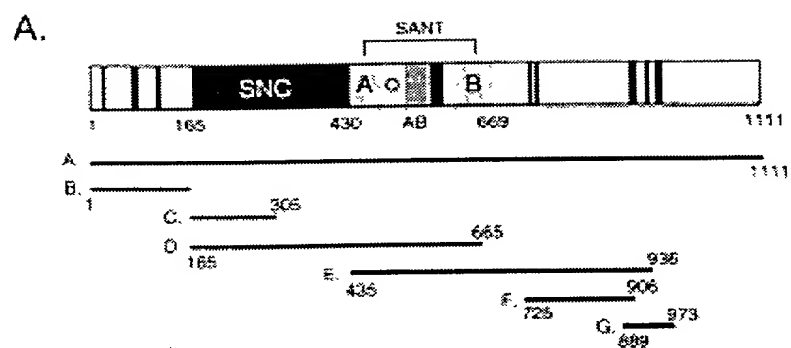


Fig. 6

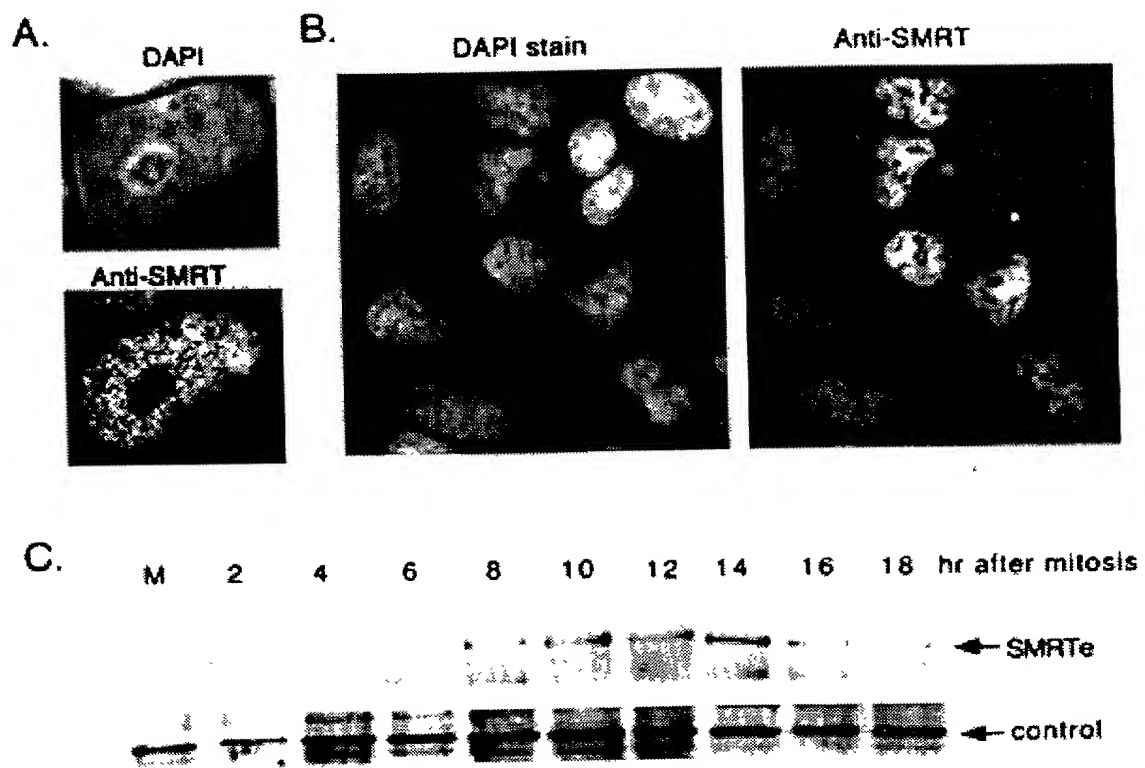


Fig. 7

